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## RAW SEQUENCE LISTING

DATE: 10/12/2001

PATENT APPLICATION: US/09/834,760

TIME: 12:10:57

Input Set : A:\19874410.app

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3 <110> APPLICANT: Austin, Richard C  
4 Chan, Anthony K.C.  
5 Berry, Leslie  
6 Hamilton Civic Hospitals Research Development Inc.  
8 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING THROMBIN  
9 GENERATION AT THE SURFACE OF CELLS  
11 <130> FILE REFERENCE: 019874-000410US  
13 <140> CURRENT APPLICATION NUMBER: US 09/834,760  
14 <141> CURRENT FILING DATE: 2001-04-12  
16 <150> PRIOR APPLICATION NUMBER: US 60/197,146  
17 <151> PRIOR FILING DATE: 2000-04-14  
19 <160> NUMBER OF SEQ ID NOS: 5  
21 <170> SOFTWARE: PatentIn Ver. 2.1  
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25 <212> TYPE: DNA  
26 <213> ORGANISM: Artificial Sequence  
28 <220> FEATURE:  
29 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer AB10230  
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52 <220> FEATURE:  
53 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer AB10232  
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62 <213> ORGANISM: Homo sapiens  
64 <220> FEATURE:  
65 <223> OTHER INFORMATION: GRP78/BiP amino acid sequence  
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69 1 5 10 15  
71 Arg Ala Glu Glu Glu Asp Lys Lys Glu Asp Val Gly Thr Val Val Gly

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72          20          25          30
74 Ile Asp Leu Gly Thr Thr Tyr Ser Cys Val Gly Val Phe Lys Asn Gly
75          35          40          45
77 Arg Val Glu Ile Ile Ala Asn Asp Gln Gly Asn Arg Ile Thr Pro Ser
78          50          55          60
80 Tyr Val Ala Phe Thr Pro Glu Gly Glu Arg Leu Ile Gly Asp Ala Ala
81 65          70          75          80
83 Lys Asn Gln Leu Thr Ser Asn Pro Glu Asn Thr Val Phe Asp Ala Lys
84          85          90          95
86 Arg Leu Ile Gly Arg Thr Trp Asn Asp Pro Ser Val Gln Gln Asp Ile
87          100          105          110
89 Lys Phe Leu Pro Phe Lys Val Val Glu Lys Lys Thr Lys Pro Tyr Ile
90          115          120          125
92 Gln Val Asp Ile Gly Gly Gly Gln Thr Lys Thr Phe Ala Pro Glu Glu
93          130          135          140
95 Ile Ser Ala Met Val Leu Thr Lys Met Lys Glu Thr Ala Glu Ala Tyr
96 145          150          155          160
98 Leu Gly Lys Lys Val Thr His Ala Val Val Thr Val Pro Ala Tyr Phe
99          165          170          175
101 Asn Asp Ala Gln Arg Gln Ala Thr Lys Asp Ala Gly Thr Ile Ala Gly
102          180          185          190
104 Leu Asn Val Met Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala
105          195          200          205
107 Tyr Gly Leu Asp Lys Arg Glu Gly Glu Lys Asn Ile Leu Val Phe Asp
108          210          215          220
110 Leu Gly Gly Gly Thr Phe Asp Val Ser Leu Leu Thr Ile Asp Asn Gly
111 225          230          235          240
113 Val Phe Glu Val Val Ala Thr Asn Gly Asp Thr His Leu Gly Gly Glu
114          245          250          255
116 Asp Phe Asp Gln Arg Val Met Glu His Phe Ile Lys Leu Tyr Lys Lys
117          260          265          270
119 Lys Thr Gly Lys Asp Val Arg Lys Asp Asn Arg Ala Val Gln Lys Leu
120          275          280          285
122 Arg Arg Glu Val Glu Lys Ala Lys Arg Ala Leu Ser Ser Gln His Gln
123          290          295          300
125 Ala Arg Ile Glu Ile Glu Ser Phe Tyr Glu Gly Glu Asp Phe Ser Glu
126 305          310          315          320
128 Thr Leu Thr Arg Ala Lys Phe Glu Glu Leu Asn Met Asp Leu Phe Arg
129          325          330          335
131 Ser Thr Met Lys Pro Val Gln Lys Val Leu Glu Asp Ser Asp Leu Lys
132          340          345          350
134 Lys Ser Asp Ile Asp Glu Ile Val Leu Val Gly Gly Ser Thr Arg Ile
135          355          360          365
137 Pro Lys Ile Gln Gln Leu Val Lys Glu Phe Phe Asn Gly Lys Glu Pro
138          370          375          380
140 Ser Arg Gly Ile Asn Pro Asp Glu Ala Val Ala Tyr Gly Ala Ala Val
141 385          390          395          400
143 Gln Ala Gly Val Leu Ser Gly Asp Gln Asp Thr Gly Asp Leu Val Leu
144          405          410          415

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146 Leu Asp Val Cys Pro Leu Thr Leu Gly Ile Glu Thr Val Gly Gly Val
147           420           425           430
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150           435           440           445
152 Gln Ile Phe Ser Thr Ala Ser Asp Asn Gln Pro Thr Val Thr Ile Lys
153           450           455           460
155 Val Tyr Glu Gly Glu Arg Pro Leu Thr Lys Asp Asn His Leu Leu Gly
156 465           470           475           480
158 Thr Phe Asp Leu Thr Gly Ile Pro Pro Ala Pro Arg Gly Val Pro Gln
159           485           490           495
161 Ile Glu Val Thr Phe Glu Ile Asp Val Asn Gly Ile Leu Arg Val Thr
162           500           505           510
164 Ala Glu Asp Lys Gly Thr Gly Asn Lys Asn Lys Ile Thr Ile Thr Asn
165           515           520           525
167 Asp Gln Asn Arg Leu Thr Pro Glu Glu Ile Glu Arg Met Val Asn Asp
168           530           535           540
170 Ala Glu Lys Phe Ala Glu Asp Lys Lys Leu Lys Glu Arg Ile Asp
171 545           550           555           560
173 Thr Arg Asn Glu Leu Glu Ser Tyr Ala Tyr Ser Leu Lys Asn Gln Ile
174           565           570           575
176 Gly Asp Lys Glu Lys Leu Gly Gly Lys Leu Ser Ser Glu Asp Lys Glu
177           580           585           590
179 Thr Met Glu Lys Ala Val Glu Glu Lys Ile Glu Trp Leu Glu Ser His
180           595           600           605
182 Gln Asp Ala Asp Ile Glu Asp Phe Lys Ala Lys Lys Lys Glu Leu Glu
183           610           615           620
185 Glu Ile Val Gln Pro Ile Ile Ser Lys Leu Tyr Gly Ser Ala Gly Pro
186 625           630           635           640
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189           645           650
192 <210> SEQ ID NO: 5
193 <211> LENGTH: 2007
194 <212> TYPE: DNA
195 <213> ORGANISM: Homo sapiens
197 <220> FEATURE:
198 <223> OTHER INFORMATION: Human GRP78/BiP mRNA sequence
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203 gaccacctac tctgcgtcg gcgtgttcaa gaacggccgc gtggagatca tcgccaacga 180
204 tcagggaac cgcatcacgc cgtcctatgt cgccttcaact cctgaagggg aacgtctgat 240
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206 gcggtcatc ggccgcacgt ggaatgaccc gtctgtgcag caggacatca agttcttgcc 360
207 gttcaagggtg gttgaaaaga aaactaaacc atacattcaa gttgatattg gaggtgggca 420
208 aacaaagaca tttgtcctg aagaaatttc tgccatggtt ctactaaaa tgaaagaaac 480
209 cgctgaggct tatttgggaa agaaggttac ccatgcagtt gttactgtac cagcctattt 540
210 taatgatgcc caacgccaag caaccaaaga cgctggaact attgctggcc taaatgttat 600
211 gaggatcatc aacgagccta cggcagctgc tattgcttat ggctgggata agagggaggg 660
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213 cattgacaat ggtgtcttcg aagttgtggc cactaatgga gatactcatc tgggtggaga 780
214 agactttgac cagcgtgtca tggaacactt catcaaactg tacaaaaaga agacgggcaa 840
215 agatgtcagg aaagacaata gagctgtgca gaaactccgg cgcgaggtag aaaaggccaa 900
216 acgggccctg tcttctcagc atcaagcaag aattgaaatt gagtccttct atgaaggaga 960
217 agacttttct gagaccctga ctogggccaa atttgaagag ctcaacatgg atctgttccg 1020
218 gtctactatg aagcccgtcc agaaagtgtt ggaagattct gatttgaaga agtctgatat 1080
219 tgatgaaatt gttcttggtg gtggctcgac tcgaattcca aagattcagc aactggttaa 1140
220 agagttcttc aatggcaagg aaccatcccg tggcataaac ccagatgaag ctgtagcgta 1200
221 tgggtgctgct gtccaggctg gtgtgctctc tggtgatcaa gatacagggtg acctgggtact 1260
222 gcttgatgta tgtccctta cacttggtat tgaaactgtg ggaggtgtca tgaccaaact 1320
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225 tcatcttctg ggtacatttg atctgactgg aattcctcct gctcctcgtg gggctccaca 1500
226 gattgaagtc acctttgaga tagatgtgaa tggatttctt cgagtgcag ctgaagacaa 1560
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**VERIFICATION SUMMARY**

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